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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/898,216

DATE: 01/25/2002

TIME: 16:58:04

Input Set : N:\Crf3\RULE60\09898216.raw

Output Set: N:\CRF3\01252002\I898216.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Hillman, Jennifer L.
Coli, Surya K.
- 8 (ii) TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
- 10 (iii) NUMBER OF SEQUENCES: 7
- 12 (iv) CORRESPONDENCE ADDRESS:
 - 13 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - 14 (B) STREET: 3174 Porter Drive
 - 15 (C) CITY: Palo Alto
 - 16 (D) STATE: CA
 - 17 (E) COUNTRY: USA
 - 18 (F) ZIP: 94304
- 20 (v) COMPUTER READABLE FORM:
 - 21 (A) MEDIUM TYPE: Diskette
 - 22 (B) COMPUTER: IBM Compatible
 - 23 (C) OPERATING SYSTEM: DOS
 - 24 (D) SOFTWARE: FastSEQ for Windows Version 2.0

ENTERED

26 (vi) CURRENT APPLICATION DATA:

- C--> 27 (A) APPLICATION NUMBER: US/09/898,216
- C--> 28 (B) FILING DATE: 02-Jul-2001
- 29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

- 32 (A) APPLICATION NUMBER: 08/781,562
- 33 (B) FILING DATE:

35 (viii) ATTORNEY/AGENT INFORMATION:

- 36 (A) NAME: Billings, Lucy J.
- 37 (B) REGISTRATION NUMBER: 36,749
- 38 (C) REFERENCE/DOCKET NUMBER: PF-0181 US

40 (ix) TELECOMMUNICATION INFORMATION:

- 41 (A) TELEPHONE: 415-855-0555
- 42 (B) TELEFAX: 415-845-4166
- 43 (C) TELEX:

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

- 49 (A) LENGTH: 356 amino acids
- 50 (B) TYPE: amino acid
- 51 (C) STRANDEDNESS: single
- 52 (D) TOPOLOGY: linear

54 (vii) IMMEDIATE SOURCE:

- 55 (A) LIBRARY: Consensus
- 56 (B) CLONE: Consensus

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Input Set : N:\Crf3\RULE60\09898216.raw
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60	Met Leu Ala Arg Ala Ala Arg Gly His Trp Gly Pro Phe Ala Glu Gly			
61	1	5	10	15
62	Leu Ser Thr Gly Phe Trp Pro Arg Ser Gly Arg Ala Ser Ser Gly Leu			
63	20	25	30	
64	Pro Arg Asn Thr Val Val Leu Phe Val Pro Gln Gln Glu Ala Trp Val			
65	35	40	45	
66	Val Glu Arg Met Gly Arg Phe His Arg Ile Leu Glu Pro Gly Leu Asn			
67	50	55	60	
68	Ile Leu Ile Pro Val Leu Asp Arg Ile Arg Tyr Val Gln Ser Leu Lys			
69	65	70	75	80
70	Glu Ile Val Ile Asn Val Pro Glu Gln Ser Ala Val Thr Leu Asp Asn			
71	85	90	95	
72	Val Thr Leu Gln Ile Asp Gly Val Leu Tyr Leu Arg Ile Met Asp Pro			
73	100	105	110	
74	Tyr Lys Ala Ser Tyr Gly Val Glu Asp Pro Glu Tyr Ala Val Thr Gln			
75	115	120	125	
W--> 76	Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys Leu Ser Xaa Asp			
77	130	135	140	
78	Lys Val Phe Arg Glu Arg Glu Ser Leu Asn Ala Ser Ile Val Asp Ala			
79	145	150	155	160
80	Ile Asn Gln Ala Ala Asp Cys Trp Gly Ile Arg Cys Leu Arg Tyr Glu			
81	165	170	175	
82	Ile Lys Asp Ile His Val Pro Pro Arg Val Lys Glu Ser Met Gln Met			
83	180	185	190	
84	Gln Val Glu Ala Glu Arg Arg Lys Arg Ala Thr Val Leu Glu Ser Glu			
85	195	200	205	
86	Gly Thr Arg Glu Ser Ala Ile Asn Val Ala Glu Gly Lys Lys Gln Ala			
87	210	215	220	
88	Gln Ile Leu Ala Ser Glu Ala Glu Lys Ala Glu Gln Ile Asn Gln Ala			
89	225	230	235	240
90	Ala Gly Glu Ala Ser Ala Val Leu Ala Lys Ala Lys Ala Lys Ala Glu			
91	245	250	255	
92	Ala Ile Arg Ile Leu Ala Ala Leu Thr Gln His Asn Gly Asp Ala			
93	260	265	270	
94	Ala Ala Ser Leu Thr Val Ala Glu Gln Tyr Val Ser Ala Phe Ser Lys			
95	275	280	285	
96	Leu Ala Lys Asp Ser Asn Thr Ile Leu Leu Pro Ser Asn Pro Gly Asp			
97	290	295	300	
98	Val Thr Ser Met Val Ala Gln Ala Met Gly Val Tyr Gly Ala Leu Thr			
99	305	310	315	320
100	Lys Ala Pro Val Pro Gly Thr Pro Asp Ser Leu Ser Ser Gly Ser Ser			
101	325	330	335	
W--> 102	Arg Asp Val Gln Gly Thr Asp Ala Ser Xaa Asp Glu Glu Leu Asp Arg			
103	340	345	350	
104	Val Lys Met Ser			
105	355			
107	(2) INFORMATION FOR SEQ ID NO: 2:			
109	(i) SEQUENCE CHARACTERISTICS:			
110	(A) LENGTH: 1188 base pairs			

RAW SEQUENCE LISTING
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111 (B) TYPE: nucleic acid
112 (C) STRANDEDNESS: single
113 (D) TOPOLOGY: linear
115 (vii) IMMEDIATE SOURCE:
116 (A) LIBRARY: Consensus
117 (B) CLONE: Consensus
119 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
121 GGCTTCTGGG AGCNACCGCT CCGCTCGTCT CGTTGGTTCC GGAGGTCGCT GCGGCCGTGG 60
122 GAAATGCTGG CGCGCGCGC GCGGGGGCAC TGGGGCCCTT TTGCTGAGGG GCTCTCTACT 120
123 GGCTTCTGGC CGCGCTCCGG CCGCGCCTCC TCTGGATTGC CCCGAAACAC CGTGGTACTG 180
124 TTCGTGCCGC AGCAGGAGGC CTGGGTGGTG GAGCGAATGG GCGGATTCCA CCGGATCCTG 240
125 GAGCCTGGTT TGAACATCCT CATCCCTGTG TTAGACCGGA TCCGATATGT GCAGAGTCTC 300
126 AAGGAAATG TCATCAACGT GCCTGAGCAG TCGGCTGTGA CTCTCGACAA TGTAACTCTG 360
127 CAAATCGATG GAGTCCTTTA CCTGCGCATC ATGGACCCTT ACAAGGCAAG CTACGGTGTG 420
128 GAGGACCTG AGTATGCCGT CACCCAGCTA GCTCAAACAA CCATGAGATC AGAGCTCGC 480
129 AAACCTCTN TGGACAAAGT CTTCCGGAA CGGGAGTCCC TGAATGCCAG CATTGTGGAT 540
130 GCCATCAACC AAGCTGCTGA CTGCTGGGT ATCCGCTGCC TNCGTTATGA GATCAAGGAT 600
131 ATCCATGTGC CACCCCGGGT GAAAGAGTCT ATGCAGATGC AGGTGGAGGC AGAGCGGCGG 660
132 AAACGGGCCA CAGTCTAGA GTCTGAGGG ACCCGAGAGT CGGCCATCAA TGTGGCAGAA 720
133 GGGAAAGAAC AGGCCAGAT CCTGGCCTCC GAAGCAGAAA AGGCTGAACA GATAAATCAG 780
134 GCAGCAGGAG AGGCCAGTGC AGTTCTGGCG AAGGCCAAGG CTAAAGCTGA AGCTATTGCA 840
135 ATCCTGGCTG CAGCTCTGAC ACAACATAAT GGAGATGCCAG CAGCTTCACT GACTGTGGCC 900
136 GAGCAGTATG TCAGCGCGTT CTCCAACTG GCCAAGGACT CCAACACTAT CCTACTGCC 960
137 TCCAACCTG GCGATGTCAC CAGCATGGTG GCTCAGGCCA TGGGTGTATA TGGAGCCCTC 1020
138 ACCAAAGCCC CAGTGCCAGG GACTCCAGAC TCACTCTCCA GTGGGAGCAG CAGAGATGTC 1080
139 CAGGGTACAG ATGCAAGTNT TGATGAGGAA CTTGATCGAG TCAAGATGAG TTAGTGGAGC 1140
140 TGGGCTTNGC CAGGGAGTCT GGGGACAAGG AACAGATTTC TCCTGATT 1188
142 (2) INFORMATION FOR SEQ ID NO: 3:
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 288 amino acids
146 (B) TYPE: amino acid
147 (C) STRANDEDNESS: single
148 (D) TOPOLOGY: linear
150 (vii) IMMEDIATE SOURCE:
151 (A) LIBRARY: Genbank
152 (B) CLONE: 31069
154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
156 Met Ala Glu Lys Arg His Thr Arg Asp Ser Glu Ala Gln Arg Leu Pro
157 1 5 10 15
158 Asp Ser Phe Lys Asp Ser Pro Ser Lys Gly Leu Gly Pro Cys Gly Trp
159 20 25 30
160 Ile Leu Val Ala Phe Ser Phe Leu Phe Thr Val Ile Thr Phe Pro Ile
161 35 40 45
162 Ser Ile Trp Met Cys Ile Lys Ile Ile Lys Glu Tyr Glu Arg Ala Ile
163 50 55 60
164 Ile Phe Arg Leu Gly Arg Ile Leu Gln Gly Gly Ala Lys Gly Pro Gly
165 65 70 75 80
166 Leu Phe Phe Ile Leu Pro Cys Thr Asp Ser Phe Ile Lys Val Asp Met
167 85 90 95

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168 Arg Thr Ile Ser Phe Asp Ile Pro Pro Gln Glu Ile Leu Thr Lys Asp
169 100 105 110
170 Ser Val Thr Ile Ser Val Asp Gly Val Val Tyr Tyr Arg Val Gln Asn
171 115 120 125
172 Ala Thr Leu Ala Val Ala Asn Ile Thr Asn Ala Asp Ser Ala Thr Arg
173 130 135 140
174 Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Lys Asn Leu
175 145 150 155 160
176 Ser Gln Ile Leu Ser Asp Arg Glu Glu Ile Ala His Asn Met Gln Ser
177 165 170 175
178 Thr Leu Asp Asp Ala Thr Asp Ala Trp Gly Ile Lys Val Glu Arg Val
179 180 185 190
180 Glu Ile Lys Asp Val Lys Leu Pro Val Gln Leu Gln Arg Ala Met Ala
181 195 200 205
182 Ala Glu Ala Glu Ala Ser Arg Glu Ala Arg Ala Lys Val Ile Ala Ala
183 210 215 220
184 Glu Gly Glu Met Asn Ala Ser Arg Ala Leu Lys Glu Ala Ser Met Val
185 225 230 235 240
186 Ile Thr Glu Ser Pro Ala Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu
187 245 250 255
188 Thr Thr Ile Ala Ala Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro
189 260 265 270
190 Ile Asp Met Leu Gln Gly Ile Ile Gly Ala Lys His Ser His Leu Gly
191 275 280 285

193 (2) INFORMATION FOR SEQ ID NO: 4:

195 (i) SEQUENCE CHARACTERISTICS:
196 (A) LENGTH: 280 amino acids
197 (B) TYPE: amino acid
198 (C) STRANDEDNESS: single
199 (D) TOPOLOGY: linear

201 (vii) IMMEDIATE SOURCE:

202 (A) LIBRARY: GenBank
203 (B) CLONE: 1065452

205 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

207 Met Asn Leu Lys Thr Cys Ser Leu Ser Thr His Ser Phe Leu Gln Lys
208 1 5 10 15
209 Lys Asn Glu Lys His Asp Gly Asn Pro Glu His Tyr Asp Thr Gly Leu
210 20 25 30
211 Gly Phe Cys Gly Trp Phe Leu Met Gly Leu Ser Trp Ile Met Val Ile
212 35 40 45
213 Ser Thr Phe Pro Val Ser Ile Tyr Phe Cys Met Lys Val Val Gln Glu
214 50 55 60
215 Tyr Glu Arg Ala Val Ile Phe Arg Leu Gly Arg Leu Ile Gly Gly Gly
216 65 70 75 80
217 Ala Lys Gly Pro Gly Ile Phe Phe Val Leu Pro Cys Ile Glu Ser Tyr
218 85 90 95
219 Thr Lys Val Asp Leu Arg Thr Val Ser Phe Ser Val Pro Pro Gln Glu
220 100 105 110
221 Ile Leu Thr Lys Asp Ser Val Thr Ser Val Asp Ala Val Ile Tyr

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Input Set : N:\Crf3\RULE60\09898216.raw
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222	115	120	125
223	Tyr Arg Ile Ser Asn Ala Thr Val Ser Val Ala Asn Val Glu Asn Ala		
224	130	135	140
225	His His Ser Thr Arg Leu Leu Ala Gln Thr Thr Leu Arg Asn Met Leu		
226	145	150	155
227	Gly Thr Arg Ser Leu Ser Glu Ile Leu Ser Asp Arg Glu Thr Leu Ala		160
228	165	170	175
229	Ala Ser Met Gln Thr Ile Leu Asp Glu Ala Thr Glu Ser Trp Gly Ile		
230	180	185	190
231	Lys Val Glu Arg Val Glu Ile Lys Asp Val Arg Leu Pro Ile Gln Leu		
232	195	200	205
233	Gln Arg Ala Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala		
234	210	215	220
235	Lys Val Ile Ala Ala Glu Gly Glu Gln Lys Ala Ser Arg Ala Leu Arg		
236	225	230	235
237	Asp Ala Ala Ser Val Ile Ala Gln Ser Pro Ala Ala Leu Gln Leu Arg		240
238	245	250	255
239	Tyr Leu Gln Thr Leu Asn Ser Val Ala Arg Glu Lys Phe Asp Asp His		
240	260	265	270
241	Leu Pro Thr Ser Asp Gly Ile Ser		
242	275	280	

244 (2) INFORMATION FOR SEQ ID NO: 5:

246 (i) SEQUENCE CHARACTERISTICS:

- 247 (A) LENGTH: 415 amino acids
- 248 (B) TYPE: amino acid
- 249 (C) STRANDEDNESS: single
- 250 (D) TOPOLOGY: linear

252 (vii) IMMEDIATE SOURCE:

- 253 (A) LIBRARY: GenBank
- 254 (B) CLONE: 1353669

256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

258	Met Glu Tyr Gly Met Pro Glu Gly Ser Tyr Asp Ser Val Phe Thr Tyr		
259	1	5	10
			15
260	Ala Pro Tyr Asn Asp Leu Asp Lys Met Gly Tyr Met Gly Pro Ala Arg		
261	20	25	30
262	Gln Gly Met Met Leu Gly Asn Lys Tyr Gly Asn Phe Thr Tyr Thr Arg		
263	35	40	45
264	Asp Tyr Gly Val Asn Met Glu Asp Asp Ile Lys Pro Leu Ser Ala Ile		
265	50	55	60
266	Glu Leu Leu Ile Phe Cys Val Ser Phe Leu Phe Val Val Met Thr Met		
267	65	70	75
			80
268	Pro Leu Ser Leu Leu Phe Ala Leu Lys Phe Ile Ser Thr Ser Glu Lys		
269	85	90	95
270	Leu Val Val Leu Arg Leu Gly Arg Ala Gln Lys Thr Arg Gly Pro Gly		
271	100	105	110
272	Ile Thr Leu Val Ile Pro Cys Ile Asp Thr Thr His Lys Val Thr Met		
273	115	120	125
274	Ser Ile Thr Ala Phe Asn Val Pro Pro Leu Gln Ile Ile Thr Thr Asp		
275	130	135	140

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/898,216

DATE: 01/25/2002

TIME: 16:58:05

Input Set : N:\Crf3\RULE60\09898216.raw

Output Set: N:\CRF3\01252002\I898216.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1